

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus.n2p model

Run on: August 22, 2003, 14:05:57 ; Search time 84 Seconds

(without alignments)
4879,442 Million cell updates/sec

Title: US-09-745-506-74

Perfect score: 2789

Sequence: 1 GTGATTGTTACTTGGTCT.....TCGTACTTACATTCACA 1553

Scoring table:

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Xgapop 10.0 , Ygapext 0.5	
Xgapop 10.0 , Ygapext 0.5	
Xgapop 6.0 , Ygapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 497079 seqs, 131961718 residues

Total number of hits satisfying chosen parameters: 994158

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB-published.Applications_AA -OFMT-fastan -SUFFIX-n2p.rapb -MINMATCH=0.1
-LOOPCL=0 -LOOEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX=10sum62
-TRANS-human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pcr -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINTEN=0
-MAXLEN=2000000000 -USER=US09745506 @cgn2_1.1.103 @runat_22082003.132713-10896
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_AA:*

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3:	/cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB.pep.*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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7:	/cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB.pep.*
8:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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10:	/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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12:	/cgn2_6/ptodata/1/pubpaa/US09C_NEM_PUB.pep.*
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14:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	366	13.1	68	9	US-09-864-761-43200	Sequence 43200, A
2	230	8.2	380	10	US-09-738-626-5952	Sequence 5952, Ap
3	218.5	7.8	287	15	US-10-156-761-13402	Sequence 13402, A
4	119.5	4.3	316	8	US-08-808-031A-45	Sequence 45, Appl
5	106	3.8	352	15	US-10-156-761-7961	Sequence 7961, Ap
6	104.5	3.7	473	10	US-09-934-899-4	Sequence 4, Appl1
7	104.5	3.7	473	12	US-09-934-868-24	Sequence 24, Appl
8	104.5	3.7	473	12	US-10-353-457-4	Sequence 4, Appl1
9	104.5	3.7	1052	15	US-10-156-761-8383	Sequence 8383, Ap
10	103	3.7	673	15	US-10-005-956-2	Sequence 2, Appl1
11	103	3.7	673	15	US-10-005-956-4	Sequence 4, Appl1
12	103	3.7	673	15	US-10-005-956-847	Sequence 847, App
13	103	3.7	673	15	US-10-005-956-857	Sequence 857, App
14	102.5	3.7	4123	15	US-10-213-509-5	Sequence 5, Appl1
15	98.5	3.5	1032	11	US-09-934-967B-6	Sequence 6, Appl1
16	98.5	3.5	1032	12	US-10-272-502A-7	Sequence 7, Appl1
17	97	3.5	488	9	US-09-815-242-11444	Sequence 11444, A
18	96.5	3.5	493	14	US-10-002-593-10	Sequence 10, Appl1
19	96.5	3.5	709	15	US-10-164-163-24	Sequence 24, Appl
20	96	3.5	691	10	US-09-919-585-6	Sequence 6, Appl1
21	96	3.5	724	10	US-09-919-585-9	Sequence 9, Appl1
22	95	3.4	1168	10	US-09-919-603-2	Sequence 2, Appl1
23	95	3.4	1172	9	US-09-919-770-4	Sequence 4, Appl1
24	95	3.4	1172	12	US-10-301-822-203	Sequence 203, App
25	95	3.4	1172	15	US-10-060-036-171	Sequence 171, Appl
26	95	3.4	1172	15	US-10-020-141-14	Sequence 14, Appl
27	95	3.4	1172	15	US-10-017-724-2	Sequence 2, Appl1
28	93.5	3.4	975	11	US-09-842-758-33	Sequence 33, Appl
29	93.5	3.4	1014	11	US-09-842-758-2	Sequence 2, Appl1
30	93.5	3.4	1014	11	US-09-842-758-32	Sequence 32, Appl1
31	93.5	3.4	1032	11	US-09-842-758-31	Sequence 31, Appl
32	93.5	3.4	1032	11	US-10-199-672-552	Sequence 552, App
33	93.5	3.4	1032	12	US-10-187-749-552	Sequence 552, App
34	93.5	3.4	1032	12	US-10-194-457-552	Sequence 552, App
35	93.5	3.4	1032	12	US-10-194-457-552	Sequence 552, App
36	93.5	3.4	1032	15	US-10-052-586-552	Sequence 552, App
37	93.5	3.4	1032	15	US-10-176-758-552	Sequence 552, App
38	93.5	3.4	1032	15	US-10-176-758-552	Sequence 552, App
39	93.5	3.4	1032	15	US-10-175-737-552	Sequence 552, App
40	93.5	3.4	1032	15	US-10-175-737-552	Sequence 552, App
41	93.5	3.4	1032	15	US-10-175-737-552	Sequence 552, App
42	93.5	3.4	1032	15	US-10-176-482-552	Sequence 552, App
43	93.5	3.4	1032	15	US-10-176-757-552	Sequence 552, App
44	93.5	3.4	1032	15	US-10-176-913-552	Sequence 552, App
45	93.5	3.4	1032	15	US-10-180-552-552	Sequence 552, App

ALIGNMENTS

RESULT 1
US-09-864-761-43200
Sequence 43200, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeonica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27

Db 237 GluTrpProTyrCysGluLeuAlaAlaGlnLeuAspGluIleSerAspArgHisGly 256
QY 1220 ATGCTGATTCCTCACTTGAGATATGATTAATATTCCTATCAGAGACTGAGAGGAC 1279
Db 257 Trp-----AspLeuArgValHisValSerIsthrValThrAsp 269
QY 1280 CCT 1282
Db 270 Pro 270
RESULT 4
US-08-808-031A-45
; Sequence 45, Application US/0808031A
; Publication No. US20020048802A1
; GENERAL INFORMATION:
; APPLICANT: Inouye, Sumiko
; APPLICANT: Hsu, Mei-Yin
; APPLICANT: Eagle, Susan
; APPLICANT: Inouye, Masayori
; TITLE OF INVENTION: PROKARYOTIC REVERSE TRANSCRIPTASE
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,031A
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 377(913).5888P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-808-031A-45
Alignment Scores:
Pred. No.: 0.00899 Length: 316
Score: 119.50 Matches: 80
Percent Similarity: 35.71% Conservative: 55
Best Local Similarity: 21.16% Mismatches: 116
Query Match: 4.28% Indels: 127
Gaps: 20
US-09-745-506-74 (1-1553) x US-08-808-031A-45 (1-316)
QY 368 CTGACCAATGACCTGACTGAGAGTGTGGAG-----GAG 403
Db 13 MetThrLysGlyPheAlaSerGluValMetArgSerProGluProIleLysTrpAsp 32
QY 404 GTGCTGCAAAAGAGGACGACCTCATTTCTCTCAACATTCGCGCTATCTCCGACCATG 463
Db 33 IleAlaLysLysGlyGlyMetArgThrIleTyrHisPro-----46
QY 464 AAGCGCATTAACCTGGAACACATGGAAGAGCGCCCTGGTGATCCGGCTCTGGAACAGA 523

Db 47 -----SerSerLysValLysLeuIleGlnTyrTrpLeuMetAsnAsn 60
QY 524 GTCCGATTCCTACTCTCTCATACAGACCTATGATGCTGGCCCGAGGGGTCAACACTGG 583
Db 61 Val-----PheSerLysLeuProMetHisAsnAlaTyrAlaPheValLysAsnArg 78
QY 584 TTGGCTAAAGGGCTTGAGCTTTGACTCCAGGCCCATACATCTCTCCAAAGCTCCCAAC 643
Db 79 SerIleLys-----SerAsnAlaLeuHisAlaGluSerLysAsnLys 93
QY 644 TAC-----CCT-----649
Db 94 TyrTyrValLysLysLeuLysAspPhePheProSerIleLysPheThrAspPheGlu 113
QY 650 -----ACAGAGGGAACACCGAGTAGAATTCACGTTAACTACACCCAGACCTG 700
Db 114 TyrAlaPheThrArgTyrArgAspArgLleGluPheThrThrGluTyrAspLysGluLeu 133
QY 701 GACAAAGTCATGTGCAAGTGAAGAAATTGACGGTGTTC-----742
Db 134 -----LeuGlnLeuIleLysThrIleCysPheIleSerAspSerThrLeuProIle 150
QY 743 -----GTCACTCTTTTCTGCTAGACGTGTAATGAGGAACA 781
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QY 782 ACAGGATTAATCTGAATTTACTCAGAGGCTTTGATGAGGTGATATTTCTTCC 841
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QY 842 CGGAACAAACACTTTATCAGACAGCAAAATTCGTCTGACTGGAGAACCTTGTCTTA 901
Db 182 AlaThrTyrThrArgTyrAlaAspAspIleIleValSerThrAsnMet-----197
QY 902 CATACTGGAATGGAGCGGTATGACACTGATGATGATGCTGCTCCGCAACATGAT 961
Db 198 ---LysGlyAlaSerLysLeu-----IleLeu 205
QY 962 GATCGAATMAAAGACACCTAAACTATCTATATTCGTTAAGCCCTTGGGTGGGAGA 1021
Db 206 AspCysPheLysArgThrMetLys-----GluIleGlyPro 217
QY 1022 ACCTTAGAGTCTCAAGTCAAGTCGTGGCCCTGTGCTGTGTTCTGGAGAGC---GTT 1078
Db 218 AspPheLysIleAsnIleLysLysPheLysIleCysSerAlaSerGlyLysIleVal 237
QY 1079 CTGCAGGCTGTGAGGCT-----GACCTTAACCTCAGAGGTGAGATGTCCCATCATGAT 1132
Db 238 ValThrGlyLeuLysValCysHisAspPheHisIleThrLeuHisArgSerMetLysAsp 257
QY 1133 ACT-----TTGATGCTGCTTCCCAAGGAATAAATGTCATCTCTGTGAACAC 1180
Db 258 LysIleArgLeuHisIleSerLeuSerLeuSerLysGlyIle-----LeuLysAspLeuAsp 275
QY 1181 AGCAACACTGAACAGCGCTTCTTCTGACCTGAGATGATGATGATTCACCTTGAG 1240
Db 276 HisAsnLysLeuSerGlyTyrIleAlaTyrAlaLysAsp---LysProHisPheTyr 294
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Db 295 ThrLysLeuAsn-----298
QY 1301 CAGAAACATCAGAGATACACATCTCTACAAATCAGCTGAGTCCCACTTAAT 1354
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RESULT 5
US-10-136-761-7961
; Sequence 7961, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO

```

1  APPLICANT:  ISHIKAWA, JUN
2  APPLICANT:  HORIKAWA, HIROSHI
3  APPLICANT:  SHIDA, TADAYOSHI
4  APPLICANT:  SAKAKI, YOSHITUKU
5  APPLICANT:  HATTORI, MASAHIRA
6  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
7  FILE REFERENCE: 249-262
8  CURRENT APPLICATION NUMBER: US/10/156, 761
9  CURRENT FILING DATE: 2002-05-29
10 PRIOR APPLICATION NUMBER: JP 2001-204089
11 PRIOR FILING DATE: 2001-05-30
12 PRIOR APPLICATION NUMBER: JP 2001-272697
13 PRIOR FILING DATE: 2001-08-02
14 NUMBER OF SEQ ID NOS: 15109
15 SEQ ID NO 7961
16     LENGTH: 3352
17     TYPE: PRT
18 ORGANISM: Streptomyces avermitilis
19 JS-10-156-761-7961

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US-09-745-506-74 (1-1553) x US-10-156-761-7961 (1-3352)

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OY	348	ATACTGTAAATAC	-----ACTCTTCGTGACCAATGACTCTAGTGAAG	392
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Db	2315	ThrvAl -GIuPhelGutPrHrvAlATgTHTu	-----Al	2327
OY	393	TGATGGAGGAGCTGCTGCAAAAAGACGACATCTCTCTACATCCGCTATCT	452	
Db	2327	AAAPGLYHISGLYVALPHEVALGIUCYSSEPTGHISPTROULEUALAASPAIALVALGL	2347	
OY	453	TCCGACCCATACGCGCATTAACCTGGAACACATGGAGAGACGCGCTGTGATCCGGCTC	512	
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Db	2347	ngLIITLeaGLuGIuTHTGILYALAAAPALVALTHCGLYSEIEIEuATgATgGLYGL	2367	
OY	513	TGGAGAACAGCTGGTATCTA	-----	534
Db	2367	ngLIgYMeTAsPArghPheLeuATgSerValSerGLuEuhISValSerGLYALHISVa	2387	
OY	535	-----	-----CTCTCTCATACAG	548
Db	2387	lAsPLeuThralAPrOheaLagLIATgPrOvalATgATgVALSPLeuPrOthITyr -A	2407	
OY	549	CCTAT	-----GATGTCGCGCCCGACGGCGTCAAC	577
Db	2407	lAPheGLnPrOGLnATgTyrTTrPLeuGLuSerAlAAsPrOvalPrOAlaGLYTHrAsPr	2427	
OY	578	-----	-----AACTGTGGCTAAAG	593
Db	2427	roVALIGUALagLIpHeTPrGLuEuaVALGIuASnThrAsPLeuSerGLYLeuAlAAsPg	2447	
OY	594	GGCTTGGAGCTTGATGCTCCAGCGCCATACATCCCTTC	-----	631
Db	2447	lulEuGLYAlAAsPAAPAlAALeUVALGIYPrOAlALeUPrOVALSerAlATrPA	2467	
OY	632	-----AAAGCTCCCACTACCTCCACAGAGGAAACACACGATAGAAATTCACGTTAACT	686	
Db	2467	rgATgATgSerATgLIuTysSerThrvAlAAsGLITrPArg-----TyrATgAlSerP	2485	
OY	687	ACACCCAAGACCTGGACAAATCATGTCTGCAGTGAAAGAAATGACGCTGTTCGTGCA	746	
Db	2485	heaTgATgLeuThrAsP-----HISAlAlAAlAPrOGLYLeuASnGLYLeuTrPLeuA	2502	

OY	747	CTCTCTTTTTCCTGAGAGCCTGTGATATGGAGAAACAACCG-----ATTAACTGAGATT	800
Db	2502	laValleuProAlaGlyLeuAlaAspGluGlnTTPAlaProCysValAlaGlyValLeuA	2522
OY	801	GTACTCGAAGAGCCTTTGATCGAGGTGTGAGATTTT-----CTTCCCGGAAACAAC	851
Db	2522	laAlaHisGlyAlaValAspValArgValAlaGluLeuProValAlaPcysAspArgSerGlnA	2542
OY	852	AACCTTTATCAGAAAGCAGAAATTTGTCTCACTGGAGAACCT-----TTGCTTTCTACATA	905
Db	2542	laAlaLysArgLeuAlaGluLeuArgGlyGluGlnProAlaGlyAlaLeuSerMetL	2562
OY	906	CTGGAAGCGAGCGGTTATGC-----ACACGTGAGTAATCTGTCCGCCGG	950
Db	2562	eugGlyLeuAlaProGlyCysHisProAlaHisProHisLeu-----SerAlaSerLeuA	2580
OY	951	CAACCATGATTTGATCGAATAAAGACACACCTAAACATATCTCAATTCGCTTACCCCTTG	1010
Db	2580	laThrThrValThrLeuLeuGln-----AlaLeuG	2590
OY	1011	GGGTGGGGAGAACCTTGAAGTCTCAAGTCAAAAGTCGTGGCCCTGTCTGCTGGGA	1070
Db	2590	ly-----AspValAspValGlnAlaProLeuTrpCysAlaThrArgGly-	2604
OY	1071	GCAGCGTTCCTCAGAGGTGTGAGCGTCAACCTTTTAACTCAGCAGGAGAGATGTCCATCATG	1130
Db	2605	--AlaValSerThrGlyValThrAspProLeu-----ArgA	2616
OY	1131	ATTACTTTGATGCTGCTGCCCAAGAGAAATTAATGTGATCCTGTGAAACAGAACACTG	1190
Db	2616	spAlaGlyGlnAlaGlnLeuTrpGlyLeuGlyValAlaAlaAlaLeuGlnLeuProAlaG	2636
OY	1191	AACGAGCGTTTCTTTCTGACCTTCGAGATTAATCGGATTTCTCACTTGGAGATAAGATTA	1250
Db	2636	rgTrpGlyGlyLeuValAspLeuProGluGlnLeuAspGluHisAlaLeuArgArgLeuA	2656
OY	1251	ATATTATTCCTATCAGAGACTCAGACAGGACCCCTTTCAAGTG	1291
Db	2656	laGlyValLeuAlaGlnHisAspGluAspGlnLeuAlaVal	2669

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: RESULT 6
: US-09-934-899-4
: Sequence 4, Application US/09934899
: Patent No. US20020102697A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Siqun
: APPLICANT: Wang, Tao
: APPLICANT: Koffas, Mattheos
: APPLICANT: Odom, J. Martin
: APPLICANT: Ye, Rick
: TITLE OF INVENTION: Genes encoding exopolysaccharide production
: FILE REFERENCE: CL1633 US NA
: CURRENT APPLICATION NUMBER: US/09/934,899
: CURRENT FILING DATE: 2001-08-22
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 4
: LENGTH: 473
: TYPE: PRT
: ORGANISM: Methylobionas 16a
: US-09-934-899-4

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Alignment Scores:	
Pred. No.:	0.336
Score:	104.50
Percent Similarity:	32.75%
Best Local Similarity:	21.83%
Query Match:	3.75%
DB:	10
Length:	473
Matches:	62
Conservative:	31
Mismatches:	88
Indels:	103
Gaps:	13

US-09-745-506-74 (1-1553) x US-09-934-899-4 (1-473)

DB 425 AlaGlnValAsnGlyTTrpArgGlyAspThrAspLeuAsnArgArgIleGluHisAspLeu 444
QY 683 AACTACACCAA 694
DB 445 TyrTyrIleGln 448

RESULT 8
US-10-353-457-4
; Sequence 4, Application US/10353457
; Publication No. US20030148494A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Siqun
; APPLICANT: Wang, Tao
; APPLICANT: Koffas, Matheos
; APPLICANT: Odom, J. Martin
; APPLICANT: Ye, Rick
; TITLE OF INVENTION: Genes encoding exopolysaccharide production
; FILE REFERENCE: CL1633 US NA
; CURRENT APPLICATION NUMBER: US/10/353,457
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US/09/934,899
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Microsoft Office 97
; SEQ ID NO: 4
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Methylobionas 16a
US-10-353-457-4

Alignment Scores:
Pred. No.: 0.336 Length: 473
Score: 104.50 Matches: 62
Percent Similarity: 32.75% Conservative: 31
Best Local Similarity: 21.838 Mismatches: 88
Query Match: 3.75% Indels: 103
DB: 12 Gaps: 13

US-09-745-506-74 (1-1553) x US-10-353-457-4 (1-473)

QY 41 AGATTGGGTGAGAAAAGTCCCTGCCG-----CACGAGACACACGCACTAG 88
DB 202 ArgLeuGlyLysLeuSerAspLeuProArgLeuValSerArgGlnAlaValAspGluVal 221
QY 89 TGGGACAGGGGTCCTGACTGAGCTTAAGTGGCTGTGCTGCTGTTTCACTGCTCG 148
DB 222 TrpValAlaPheProGlyAlaSerLeuAlaGluArgValGln----- 235
QY 149 GAAAGGCGCTGAAGTGGCACTGAAATGAGCATAGATGATCCCGACAGACATCCGTTT 208
DB 236 -----HisGluLeuArgHis-----LeuProValSerIleArgLeu 247
QY 209 GTAGATTCCTCGATGTGCATTTCTCCCTTCCTTCANGATTGAAGCTTCCTTCT 268
DB 248 ValIleAspCysPheAlaPheLysGlnSerLysPheLeu----- 260
QY 269 TCCTTGATGACTTTCGATCCCTCTCGTTTGGTGAAGCTGGGACAATGTGATTAAG 328
DB 261 SerLeuAsnThrValAlaGlyLysLeuProThrLeuAsp----- 272
QY 339 GTGGAACAGACCCACCATACTACTTAATATACACTTTCCTACACAAATGACCTGACTAG 388
DB 273 ValSerValSerProLeuHisGlyValAsnArgTyrIle-----Lys 286
QY 389 GAAGTGAATGGAGAGAGTGTCTCAAAAAGAGCAAGCTCATTT----- 430
DB 287 GluIleGluAspArgLeuValAlaLeuLeuLeuLeuLeuIleSerProLeuMetLeu 306
QY 431 -----CTCTCTACCATTCGCGCTATGCTTCGAGCCATGAAGGCG 469
DB 307 ValIleAlaLeuGlyValLysLeuSerSerProGlyProValPheTyrLysGlnValArg 326
QY 470 ATAACCTGGAACATGGAAGAGGCGCTGTGT----- 502

DB 327 ValGlyTTrpAsnAsnArgLysPheThrMetLeuLysPheArgSerMetProValAspAla 346
QY 503 -----ATCCGGGCTCTGGACAGAGATC-----GGT 529
DB 347 GluAlaLysThrGlyAlaValTrrpAlaArgProGlyGluAsnArgAlaThrArgPheGly 366
QY 530 ATCTACTCTCTCATATACAGCTATGATGCTGGCGCCGACAGGCGTCAACAAGTGTGGCT 589
DB 367 AlaPheLeuAlaGlyThrSerLeuAspGluLeuProGlnLeuIleAsn-----ValLeu 384
QY 590 AAGGG-----CTTGAGCTTGTACTTCAGGCC-----ATACAT 625
DB 385 LysGlyAspMetSerLeuValGlyProArgProGluArgProAspPheValGluValPhe 404
QY 626 CCTCCAAAGCTCCCACTAC----- 646
DB 405 LysAspGlnValProAsnTyrMetLysHisMetValLysAlaGlyIleThrGlyTyr 424
QY 647 -----CCTACAGAGGGAACACGAGTACATTCACAGTT 682
DB 425 AlaGlnValAsnGlyTTrpArgGlyAspThrAspLeuAsnArgArgIleGluHisAspLeu 444
QY 683 AACTACACCAA 694
DB 445 TyrTyrIleGln 448

RESULT 9
US-10-156-761-8383
; Sequence 8383, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OKURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIZAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRU
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO: 8383
; LENGTH: 1052
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8383

Alignment Scores:
Pred. No.: 0.495 Length: 1052
Score: 104.50 Matches: 99
Percent Similarity: 33.26% Conservative: 57
Best Local Similarity: 21.11% Mismatches: 188
Query Match: 3.75% Indels: 125
DB: 15 Gaps: 20

US-09-745-506-74 (1-1553) x US-10-156-761-8383 (1-1052)

QY 11 TCTTGTGCTGCAGAGACAGACAGAAAGAGATGGGTCAAGAAAAGTCCCTGCCGCAK 70
DB 362 SerTyrCysTrpLeuLysSerAlaLysProAsnIleGlyHisLeuAspAla----- 378
QY 71 CAGAGACAGCGGACACTAGTGGGACAGGGTCTCGATCAGACTTAAGTTCGCTGTCTCG 130
DB 379 -----AlaAlaGlyIleAlaGly 384
QY 131 TGGTTTCACTGTCTCGGAAAAGGCTGAGTGGCACTGAATGAGGACATGATGATGTC 190

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Db      385 LeuileysThrValLeu-----SerLeuLysAsnArgLysVal 397
QY      191 CCCACGACGATCCGCTTT-----GTGATTTCCCTCATCTGC 226
Db      398 ProProValValaAnPheArgArgProAsnProLysLeuAlaLeuAspSerSerProPhe 417
QY      227 AATTTCCCGCTCCCTTCATGATTTGAAGCT-----CTCCCTTCTCTTGAT 277
Db      418 ArgValAlaThrGluLeuThrArgLeuGluGluAspGluProLeuAlaLeuSerValAsn 437
QY      278 GACTTTGCATCCCTGCTGTTGCTGAGAGTTGGGACATGTGGATTCGTGCGAACA 337
Db      438 -----SerLeuAlaMetGlyGlyThrAsnAlaHisValValLeuGluGlu 452
QY      338 AGCCACACA-----CATCTGTAAATACACTC 364
Db      453 AlaProProValArgSerGlyGlyAlaSerArgArgArgHisProVal----- 469
QY      365 TTCTGTACCAATGACCTGACTGAGAGAGTATGGAGAGGTGCTGCAAAAG----- 415
Db      470 ---LeuLeuSerAlaLysSerGlyGluAlaLeuGluAspLeuSerGlnSerLeuGlyGln 488
QY      416 -----AAGCAGACCTCATCTCTCTCCATCCGCTATCTTCGCA 457
Db      489 TPAlaArgGluAsnProHisAlaAspValAlaAspValAlaHis----- 503
QY      458 CCCATGAAGCCATTAACCTGGACACATGGAAGAGCCGCTGTGATCCGGCTCTGGAG 517
Db      504 -----ThrLeuAlaThrGlyArgGluLeuProLeuAlaArg----- 516
QY      518 AACGAGTCGGTATCTACTCTCCAT-----ACAGCTATGATGCTGCGCC 565
Db      517 -----AlaLeuThrAlaHisAspLeuAspValAlaLysGlyLeuSerThr 532
QY      566 CAGGCGCTGACACACTGGTTG---GCTAAGGCGCTTGAGCTTACTCCAGGCCCAT 622
Db      533 ArgGlySerArgSerGlnArgGluAlaGlnAlaArgLysValArgThrAlaPheLeu 552
QY      623 CATCTTCCAAAGCTCCCACTACCTACACAGAGGGAACCAACCGATGAATTCACGTT 682
Db      553 PheProGlyGlnGlyThrGlnLeuProAlaMetGlyAlaArgLeuAlaGlnGlyAspPro 572
QY      683 AACATACACCCAAAGCTGAGCAAGTCACTGTCTGCAAGCAAA-----GGAATTGAC 733
Db      573 ValPheAlaAlaHisLeuAspArgValIleGlyLeuPheGlnGluArgAlaGlyValAsp 592
QY      734 GGTGTTCTGCTCACTTTTCTGCTAGAGCTGATAGGAGCAACAACGGATTAT 793
Db      593 LeuLeuProValAlaLeuArgProAspAlaSerThrLeuGluGluAlaArgThrThrLeuThr 612
QY      794 ---CTGAATTGCTACAGAGGCTTTGATGCAGGTGATGATTTTCTTCCGGAACAA 850
Db      613 AlaThrGluGlyThrGlnProAlaLeuPheAlaValAlaGluThrPalaLeuGlyArgThrLeu 632
QY      851 CAACTTATCGAAGAGCGAAATTTCTCACTGCGAAGACCTTGCTTCTCAATACATGGA 910
Db      633 MetAspTyr-----GlyValArgProTyrAlaMetLeuGlyHisSer 946
QY      911 ATGGAGCGGTTA-----TGACACTGSGATGAATCTGCTCCCGCAACCATGATTAT 964
Db      647 ValGlyGluLeuValAlaAlaThrLeuGlyGlyValLeuAspPheAlaProAlaValGlu 666
QY      965 CGAATTAAGACACCTTAACCTATCTCATATTGCTTACGCTTGGGGGAGAGACC 1024
Db      667 LeuValAlaArgArgGlyArgLeu-----MetSerGluThr 678
QY      1025 TTAGAGTCTCAAGTCAAGGCTGGGCGCTGTGCTGCTTGGAGACGCGTTCTCGAG 1084
Db      679 ProGlyGluAlaMetLeuTyrValAsnLeuAlaGluGluAlaAlaLysLeuLeuAsp 698
QY      1085 GGTGTTAGGCTGACCTTACCTC-----ACA 1111

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Db      699 AspValProGlyAspLeuThrLeuAlaAlaValAsnAlaAspGlnLeuValValSer 718
QY      1112 GGTGAGATGTCCTCATCATGATCACTTGTGATGCTGCTCCCAAGAAATAATGTCATCCTC 1171
Db      719 GlyAlaProGlnGluValGluGluLeu---AlaAlaArgLeuArgAlaAspGlyValSer 737
QY      1172 TGTGAACACACCAACACTGAAACGAGGCTTCTTCTGACCT----- 1213
Db      738 CysGlyArgLeuGluValThrArgAlaPheHisSerProLeuMetAspThrAlaAlaAsp 757
QY      1214 -----CGAGATATGCTGATTCAC 1234
Db      758 ThrPheArgGlnAlaAlaAspSerHis 766

RESULT 10
US-10-005-956-2
; Sequence 2, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT FILING DATE: 2001-12-03
; PRIOR FILING DATE: 2000-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 673
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-005-956-2

Alignment Scores:
Pred. No.: 0.561 Length: 673
Score: 103.00 Matches: 98
Percent Similarity: 36.18% Conservative: 67
Best Local Similarity: 21.49% Mismatches: 159
Query Match: 3.69% Indels: 132
Gaps: 23

US-09-745-506-74 (1-1553) x US-10-005-956-2 (1-673)
QY      9 TATCTTGGTGGCGACAGAGACAGAGAGAGATTGGTGCAGAAAACCTGCCCTGCCGC 68
Db      81 TTTTGGTGGTGGCGACAGAGACAGAGAGAGATTGGTGCAGAAAACCTGCCCTGCCGC 92
QY      69 AACAGACACAGCGCATAGTGGAGAGAGGCTGCTGACTCAAGACTTAAGCTGCTG--- 125
Db      93 ThrGlyPheThrGlySerLeuGlyThrAlaValAlaThrMetLysLysAlaAlaValThr 112
QY      126 -----TCTGCTGTTTTCACCTGCTCTGGAAGAGCGCTGGAAGCTGGAAGCTGAATGAGGC 179
Db      113 ThrAspSerArg--TyrThrPheGlnAlaGluArgGlnMetAspLysAsnThrGluLeu 132
QY      180 ATAGATGAGTCCCAACAGCA-----GTCCGCTTGTGATTCCTGATTCCTGCAATTCCT 233
Db      132 TslYsGluValGlyThrThrProIleValThrThrPheLeuThrGluIleProAlaGlyG 152
QY      234 CCCGCTCTTCATGAGATTGAAGGCTCCCTTCTCTCTGTAATGACTTTGCATCCCTCT 293
Db      152 LysArgValGlyPheAsp---ProPheLeuLeuSer----- 162
QY      294 CGTTTGTCTGAGAGTGGAGCAATGTGGATTAAGTGTGGAACCAAGCCACCATTAAGT 353
Db      163 -----TlaAspThrThrPheLysTyrAspLeuAlaLeuGlnGlySerAsnArgGlnLeu 181
QY      354 TAAATACACTCTTCTCTGACCAATGACCTGACTGAGAGAAAGTATGAGAGAGGTGCTGCAA 413

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Db      181 alser-----ilethrthrasnleu-----187
QY      414 AGAAGCAGACCTCATCTC--TCCTACCATCC-----CCTATCTCC 455
Db      188 -----valaspleuvaltrpglysergluarproprovalproanglnproiletyla 206
QY      456 GAACCATGAAGGCATACCTGGACATGGAAGAGCGCGGAGATCCGGGCTGG 515
Db      206 lalenglnglnalaphethrlyserthrtrpglnglnlysal-----220
QY      516 AGAACAGAGTCGGTATCTACTCTCTCATACACAGCTATGATCGTCCGCCAGGCGTC- 574
Db      221 -----serglyvalargserglmetelnyshsglnlysalprothralaval 238
QY      575 -----AACACTGGTGGCTAAAGGCGTTGAGCTTGACTCCCA 614
Db      238 euleuseralaleuglnglnthrtralaThrleupheasn-----250
QY      615 GGCCCATACATCCTCCCAAGCTCCCAAGCTACACCTACAGAGGAAACACCGAGTAGAAT 674
Db      251 -----leuargalaserasplleprotyrasnpro-----p 261
QY      675 TCACACCTTAACCTACACCCCAAGACCTGACAAAGTCACTGTCGACGTGAAGAGAAATGACG 734
Db      261 hepethrlyserlythrleuThrleuthrasp-----Sers 272
QY      735 GTGTTCTCTGCTACTTCTTTTCTGCTAGACGTGATATGAGAACAAACCGATTATC 794
Db      272 erlleargleuphealasnlyserargphesergergluthrleuserlytleuasn 292
QY      795 TGAATGTACTCTGAGAGCGTTGATGACAGTGTAGATTTT-----835
Db      292 eserctythrtrglyprometcyasalnglnleuasptrysergluvalargasert 312
QY      836 -----CTTCCCGGAAACAAACTTTATC 860
Db      312 leglinaltyrserleuglyasprvalargilertrplegllythrserlythrmetyrg 332
QY      861 AGAAGCAGAAATCTGCTACCTGAGAGACCTTGCTTCTACTACTGGAATGGAGCGT 920
Db      332 lytletryglumetleproargglulys-----341
QY      921 TATGACACTGATCTGATCTGCTCCCTGACACCATGATGATGATCAATTAAGAACAC- 979
Db      342 -----leuvalthrappthrlyserprovalmetethrlysalavalylasnsert 360
QY      980 -----CTAAACTATCTCATATTCCTTAGCCCTTGGGGTGGGAGA--- 1021
Db      360 ysglnglnalaleuLeuLysalaserhisvalargaspralavalaleargtyl 380
QY      1022 -----ACCTTAGAGTCAAGTCAAAAGTGTGGCGCTGTGTGCTGCGGAGCAGCG 1076
Db      380 euvaltrpleuglnlysalasnvalprolysglythrvalasprglupheserglyalut 400
QY      1077 TTCTGAGGAGGTGTGGAGCTGACCTTACCTACAGAGGTGAGATGCCATCATGATACTT 1136
Db      400 levalasprlyshearaglyglnglnglnphesergerglyproser---Phegluthr 419
QY      1137 TGGATCTGCTCTCCCAAGGAATTAATGTCATCTCTGTGAACACAGCAACTGAA--- 1192
Db      419 leseralaser-----glyleuasnalaalaleuLanhlstylyserProcthrlysgln 437
QY      1193 -----CGAGGCTTCTTCTGACCTTCGAGATATGCTGATTC 1231
Db      437 euaasnarglyleuserSeraspglumetlyrleuLeuaspSer 451

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; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 673
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-005-956-4

Alignment Scores:
Pred. No.: 0.561 length: 673
Score: 103.00 matches: 98
Percent Similarity: 36.18% conservative: 67
Best Local Similarity: 21.49% mismatches: 159
Query Match: 3.69% indels: 132
DB: 15 gaps: 23

US-09-745-506-74 (1-1553) x US-10-005-956-4 (1-673)
QY      9 TATCTTGCTGCTCAGACAGACAGACAGAGAGGAGATTGGTCAAGAAACTGCCCTGCCG 68
Db      81 Tyrilegly---glnhlsasprgluarargala---trple-----92
QY      69 ACAGAGACAGAGGCGCTACTATGGGACAGGGGCTCTGACTACAGATTAACTGCTGTG--- 125
Db      93 ThrlypnehrthrlyseralaglythrtralaValalThrmetlysalalaalvaltrp 112
QY      126 -----TCTGCTGATTTTCTACTGCTCTCGAAGAGCGCTGAGTGCATGAATGAGCG 179
Db      113 Thraspserarg---tyrtrpThrlnalaglnuarglnmetabpcysasntrpgleuuh 132
QY      180 ATAGATGAGTCCCGACGACA-----GTCCGTTTGTAGATTCCTGATCTGCAATTCCTT 233
Db      132 lslsglnuvalglythrThrProilvalthrtrpleuThrnglnleProalagl 152
QY      234 CCCGTCCTTCATGAGATTGAAGCTCTCTCTCTCTCTCTGTAATGACTTGATTCCTCT 293
Db      152 lyargvalglyheasp---ProphleuLeuuser-----162
QY      294 CGTTTGTGAGAGTGTGGACAAATGTGATTAAGTGTGGAACCAAGCCACACATACTG 353
Db      163 -----lleasprthrtrpglyserlytraspheunlaleuglnglyserasnarglnleu 181
QY      354 TAAATTAACCTTCTCTGACCAATGACCTGACTGAGAGATGAGAGAGGAGTCTGCATA 413
Db      181 alser-----ilethrthrasnleu-----187
QY      414 AGAAGCAGACCTCATCTC--TCCTACCATCC-----CCTATCTCC 455
Db      188 -----valaspleuvaltrpglysergluarproprovalproanglnproiletyla 206
QY      456 GAACCATGAAGGCATACCTGGACATGGAAGAGCGCGGAGATCCGGGCTGG 515
Db      206 lalenglnglnalaphethrlyserthrtrpglnglnlysal-----220
QY      516 AGAACAGAGTCGGTATCTACTCTCTCATACACAGCTATGATCGTCCGCCAGGCGTC- 574
Db      221 -----serglyvalargserglmetelnyshsglnlysalprothralaval 238
QY      575 -----AACACTGGTGGCTAAAGGCGTTGAGCTTGACTCCCA 614
Db      238 euleuseralaleuglnglnthrtralaThrleupheasn-----250
QY      615 GGCCCATACATCCTCCCAAGCTCCCAAGCTACACCTACAGAGGAAACACCGAGTAGAAT 674

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RESULT 11
; Sequence 4, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company

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Db 332 lylletryglumetileproarglulys----- 341
Qy 921 TATGCACACTGATGATGTCTCCCTGGCAACATGATGATGATAAAGACAC- 979
Db 342 -----LeuValThrSprThrTyrSerProValMetMetThrLysAlaValLysAsnSerL 360
Qy 980 -----CTAAACATATCTCATATTCGCTTACCCCTGGGCGGGGAGA----- 1021
Db 360 ysglglalalaleuleuLysAlaSerHisValAlaTgspAlaValAlaValIleArgTyrL 380
Qy 1022 -----ACCTTAGACTCTCAAGTCAAGTCGTGGCCCTGTGTCTGTCTGTGGAGCAGC 1076
Db 380 euValTyrPleuglulysAsnValProlysglYThrValaspLupheseSerGlyAlaGluI 400
Qy 1077 TTCTGCAGGCTGTGAGCTGACCTTTACCTCAGAGGTAGATGTCCCATCATGATCTT 1136
Db 400 leValAspLysPheArgglugluglunPheSerSerGlyProSer---PheGluThrI 419
Qy 1137 TGGATGCTGCTCCCAAGAAATAATGTATCTCTGTGACACAGACACACTGAA----- 1192
Db 419 leSerAlaSer-----GlyLeuAsnAlaAlaLeuAlaHisTyrSerProThrLysGluI 437
Qy 1193 -----CGAGGCTTCTTCTTGACCTTGACATATGCTGATTCCT 1231
Db 437 euAsnArgLysLeuSerSerAspGluMetTyrLeuLeuAspSer 451

RESULT 13

US-10-005-956-857
; Sequence 857, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005, 956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251, 015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263, 678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273, 037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 857
; LENGTH: 673
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-005-956-857

Alignment Scores:

Pred. No.: 0.561 Length: 673
Score: 103.00 Matches: 98
Percent Similarity: 36.18% Conservative: 67
Best Local Similarity: 21.49% Mismatches: 159
Query Match: 3.69% Indels: 132
Gaps: 23

US-09-745-506-74 (1-1553) x US-10-005-956-857 (1-673)

Qy 9 TATCTTGATGCTGCAGAGACAGACAGAGAGATGGTCAGAAAGCTCCCTCCGC 68
Db 81 TyrIleGly---GlnHisAspGluArgAlaGala---Trrile----- 92
Qy 69 ACCAGAGCAGACGACACTAGTGGGACAGGGGCTCTGACTCAGACTTAAGTCTGTG-- 125
Db 93 ThrGlyPheThrGlySerIleGlyThrAlaValAlaValIleThrMetLysAlaAlaValTrr 112
Qy 126 -----TTCGTGGTGTTCACATGCTCTGAAAGCCCGAAGTGGCACTGAATAGGC 179
Db 113 ThrAspSerArg---TyrTrrPheGlnAlaGluArgIleMetAspCysAsnTrrPgluLeuH 132

Qy 180 ATAGATGAGTCCCAAGACAGAC-----GTCCGGTTGTAGATTCCCTGATCTGCATTTCT 233
Db 132 lEysgluValIglYThrThrProIleValThrTrrPheuLeuThrGluIleProAlaGlyG 152
Qy 234 CCCGTTCCCTCATGATGATTTGAAGGCTCTCCCTTCTCTCTGAAATGACTTTGCATCCCTCT 293
Db 152 lYArgValGlyPheAsp---ProPheLeuLeuSer----- 162
Qy 294 CGTTTCTGAGAGTTGGGACATGTGGATTACTGATGATGACCAACCAACCACTACTG 353
Db 163 -----lLeasPThrTrrPgluSerTyrAspLeuAlaLeuGlnGlySerAsnArgGlnLeu 181
Qy 354 TAAATACACTCTCCGACCAATGACCTGACTGAGAGATGATGAGAGAGTGTCTGCATA 413
Db 181 alSer-----lIeThrThrAsnLeu----- 187
Qy 414 AGAAGCAGACCTCATATTC---TTCATACATCCG-----CTATCTTCC 455
Db 188 -----ValAspLeuValTrrPglYserGluArgProProValProAsnGlnProIleTyrA 206
Qy 456 GACCCATGAAGCCATTAACATGAGACATGAGAGAGGCGCTGGATCCGGGCTCTGG 515
Db 206 lAlauglulAlaPheThrGlySerThrTrrPgluIulysVal----- 220
Qy 516 AGAACAGAGTGGGTATCTACTCTCTCATATACAGCTATGATGCTGCGCCCAAGGCGTC- 574
Db 221 -----SerGlyValArgSerGlnMetGlnLysHisGlnLysValProThrAlaValI 238
Qy 575 -----AACACTGTTGGCTAAAGGCTTGAGCTTGTACTTCA 614
Db 238 euLeuSerAlaLeuGluGluThrAlaTrrPheuPheAsn----- 250
Qy 615 GGGCCATACATCTTCCCAAGCTCCCACTACCTTACAGAGGAACCAACCGATGAAT 674
Db 251 -----LeuArgAlaSerAspIleProTyrAsnTr-----P 261
Qy 675 TCACAGTTACTACACCCCAAGACCTGAGCAAAAGTCAATGTCATGTCAGTGAAGAAATGACG 734
Db 261 hePheTyrSerTyrTrrIleLeuLeuThrAsp-----Sers 272
Qy 735 GTGTTTCTGACTTCTTTTTCGTAGACGTGTAATGAGAACAAACGATTAATC 794
Db 272 erlLeArgLeuPheAlaAsnLysSerArgPheSerSerGluThrLysSerTyrLeuAsnS 292
Qy 795 TGAATGTACTCAGAAAGGCTTGTGATGACAGTGTAGATTTT----- 835
Db 292 erSerCysThrGlyPrometCysValGlnlIleGluAspTyrSerGlnValArgAspSerI 312
Qy 836 -----CTTCCCGGAACAAACTTATC 860
Db 312 lGlnAlaTyrSerLeuGlyAspValArgIleTrrPleGlyThrSerTyrThrMetCyrG 332
Qy 861 AGAAGACGGAATTCGTCTGCTGAGAGACCTTGTCTTACATACTGGAATGGACGGT 920
Db 332 lylletryglumetileproarglulys----- 341
Qy 921 TATGCACACTGATGATGTCTCCCTGGCAACATGATGATGATAAAGACAC- 979
Db 342 -----LeuValThrSprThrTyrSerProValMetMetThrLysAlaValLysAsnSerL 360
Qy 980 -----CTAAACATATCTCATATTCGCTTACCCCTGGGCGGGGAGA----- 1021
Db 360 ysglglalalaleuleuLysAlaSerHisValAlaTgspAlaValAlaValIleArgTyrL 380
Qy 1022 -----ACCTTAGACTCTCAAGTCAAGTCGTGGCCCTGTGTCTGTGGAGCAGC 1076
Db 380 euValTyrPleuglulysAsnValProlysglYThrValaspLupheseSerGlyAlaGluI 400
Qy 1077 TTCTGCAGGCTGTGAGCTGACCTTTACCTCAGAGGTAGATGTCCCATCATGATCTT 1136
Db 400 leValAspLysPheArgglugluglunPheSerSerGlyProSer---PheGluThrI 419
Qy 1137 TGGATGCTGCTCCCAAGAAATAATGTATCTCTGTGAAACACACACTGAA----- 1192

Db 419 IeserAlaser-----GlyLeuAsnAlaAlaLeuAlaHisTyrSerProThrLysGluL 437
QY 1193 -----CGAGGCTTTCTTTCGACCTTCGAGATATGCTGATTC 1231
Db 437 euAsnArgLysLeuSerSerAspGluMetTyrLeuAspSer 451

RESULT 14
US-10-213-509-5
: Sequence 5, Application US/10213509
: Publication No. US20030054485A1
: GENERAL INFORMATION:
: APPLICANT: Weiss, Joseph
: APPLICANT: Scott, Matthew
: TITLE OF INVENTION: JELLY BELLY GENES AND THEIR USES
: FILE REFERENCE: STAN-232
: CURRENT APPLICATION NUMBER: US/10/213,509
: PRIOR FILING DATE: 2002-08-06
: PRIOR APPLICATION NUMBER: 60/311,720
: PRIOR FILING DATE: 2001-08-09
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 4123
: TYPE: PRT
: ORGANISM: H. sapiens
US-10-213-509-5

Alignment Scores:
Pred. No.: 1.51 Length: 4123
Score: 102.50 Matches: 106
Percent Similarity: 27.31% Conservative: 36
Best Local Similarity: 20.38% Mismatches: 157
Query Match: 3.72% Indels: 221
Gaps: 25

US-09-745-506-74 (1-1553) x US-10-213-509-5 (1-4123)

QY 1406 CCTCGAAGACACTCTCTGGAAGACACACCTCCACTGATGTTACAATTAAAT 1347
Db 1333 ProIasSerThrLeuProGlyProSerPro-----GlySerLeuAsp 1346
QY 1346 TGGGATCCAGCTGATTTGTGAAGATGCTATGCTGATGTTCTGCAATTATACCACCT 1287
Db 1347 ThrIasSer-----ProLeuAlaSerAlaSerProAlaPro 1359
QY 1286 GAAGAGGCTCCCTGACTCTCTGATAGATAATATTATCTATTCACAAGTGAAT 1227
Db 1360 ProCysGlyProPheGluPheArgCysGly----- 1369
QY 1226 CCAGCATATCTGGAAGGTCAAGAAAGCCTGTTGAGTGTGCTGTTCACAGAGA 1167
Db 1370 -----SerGlyGlu-----CysThrProArgGly 1377
QY 1166 TGACATTTATCTTGGGAGAGACAGATCAAGTATCATGATGGACATTCACCTGCA 1107
Db 1378 -----TrrPArgCysAspGlnGluAspCysAlaAspGlySerAspGluArg--- 1393
QY 1106 GGTAAAGGTCAAGCTCAACACCTGTCAGAACGC--TGCCTCCAGAACACAGACAGAGG 1050
Db 1394 GlyCysGlyGlyProCysAlaProHisAlaProCysAlaArgGlyProHisGly--- 1412
QY 1049 CCAGACTTTGACTTGAGACTCTAAGGTTCTCCCAAGGAGGCTAAGCGAATATGAG 990
Db 1413 -----ValSerProGluGln 1417
QY 989 ATAGTTTAAAGTCTTTTATTCGATCATCATGTTGCCAGGAGACAGATTATCA 930
Db 1418 LeuCysAspGlyVal-----ArgGlnCysProAsp 1427
QY 929 GTGTGATTAACCGTCCTTCATTCAGATGTAGAACGAAGGCTTTCAGTGCACAGATT 870
Db 1428 GlySerAspGluGlyProAspAlaCysValGluAlaProAlaProProAlaMetArgGly 1447

QY 869 CCGTCTTGATTAAGTTGTTGTTCCGGAAAGAAATGTAACCACTGATCAAAAGCT 810
Db 1448 ProProGluGln-----AlaGlyGlyProThrSerArgAlaProSerProPro 1464
QY 809 TCTGAGTACATTCGATTAATCCGTGTTTGTCTCTATACCACTCTAGCAAGAAAG 750
Db 1465 SerPro-----ProGluAlaGlnGlyGlyArgLys 1475
QY 749 AAGTCAGAAACACCTCAATTCCTT-----TCACTCAGACATGACTT 705
Db 1476 GlyGlnGluArgSerArgThrHisLeuThrValProAlaGlySerThrGlnLeuProLeu 1495
QY 704 TGTCCAGCTCTGGGTAGTTAAAGTGAATTACTGCGGTTCCTCTGTAGGCT 645
Db 1496 CysProGlyLeu-----PheProCys----- 1502
QY 644 AGTTGGAGCTTTGGAAGATGTATGGCCTCGAGGTACAAAGCTCAAGCCCTTACGCA 585
Db 1503 -----GlyValAlaPro 1506
QY 584 ACCAGTTGTACCGCTGGGGCGCAGCATATAGCTGTATGAGAGATGATACCGCA 525
Db 1507 GlyLeuCysLeuThrPro-----GluGln 1514
QY 524 CTCTGTTCTCCAGAGCCCGATCACCA----- 498
Db 1515 LeuCysAspGlyIleProAspCysProGlnGlyAspGlyLeuAspCysGlyGlyLeu 1534
QY 497 -----GGCGCTCTGCATGCTGTCCAGTTATGCGCTCATG- 459
Db 1535 ProAlaLeuGlyGlyProAsnArgThrIleLeuProCysProGlyIleThrCysProAsn 1554
QY 458 -----GTGCGA-----AGATAGCGGATGGTGAAGAGATGAGTCTGCTCT 414
Db 1555 GlyThrCysIleGlyPheGlnLeuValLeuCysAspGlyGlnProAspCysGlyArgProGly 1574
QY 413 TTTCAGACACCTCTCCATCTCTCTGACAGCTCATGG----- 372
Db 1575 GlnValGlyProSerProGlnGlnGlnGlyCysGlyAlaIleArgIleProThrSerProThr 1594
QY 371 -----TCAGAGAGCTGATTTACAGTATGTG 345
Db 1595 GlyProCysSerArgThrCysGlyProThrGlyGlnGlyArgSerArgArgCysSerPro 1614
QY 344 GTGGGCTTGTTCCACAGTAATCCACATTCCTCCAAAC----- 306
Db 1615 LeuGlyLeuLeu-----ValLeuGlnAsnCysProGlyProGlnHisGlnSerGlnAla 1632
QY 306 ----- 306
Db 1633 CysPheThrAlaAlaCysProValAspGlyLeuIleThrSerThrTrpSerProThrSerVal 1652
QY 305 ---PCTCAGCAAGAGAGGGATGCAAGTCAATTCAGAGAAAGAGAGAGCTCAAT 249
Db 1653 CysSerGluProCysArgGlyThrMetThrArgGlnArgGlnCysHisSerProGlnAsn 1672
QY 248 CCATTAAGAAAGGAGAAATTCAGATCAGAGGAATTAACAACCGAGTGTGTGGGA 189
Db 1673 -----GlyGlyArgThrCysAlaAla----- 1679
QY 188 CTCATCTATGCTCATTTTCAGTGCACCTTCAGAGCCCTTTTCCAGAGCACTGAAAAACAG 129
Db 1680 -----LeuProGlyGlyLeuHisSerThr 1687
QY 128 AGACAGCAGCAAGTTAAGTCTGAGTCAGACCCCTGTCCAGTAAAGGCTGCTGCT 69
Db 1688 ArgGlnThrLys---ProCysProGlnAspGlyCysPro---AsnAlaThrCysSerGly 1705

RESULT 15
US-09-954-987B-6
: Sequence 6, Application US/09954987B
: Publication No. US20030104523A1

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GENERAL INFORMATION:
APPLICANT: Stefan Bauer
APPLICANT: Grayson B. Lipford
APPLICANT: Hermann Wagner
TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
FILE REFERENCE: C1041/7016 (AMS)
CURRENT APPLICATION NUMBER: US/09/954,987B
PRIORITY FILING DATE: 2001-09-17
PRIORITY APPLICATION NUMBER: US 60/233,035
PRIORITY FILING DATE: 2000-09-15
PRIORITY APPLICATION NUMBER: US 60/263,657
PRIORITY FILING DATE: 2001-01-23
PRIORITY APPLICATION NUMBER: US 60/291,726
PRIORITY FILING DATE: 2001-05-17
PRIORITY APPLICATION NUMBER: US 60/300,210
PRIORITY FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 230
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 1032
TYPE: PRT
ORGANISM: Homo sapiens
US-09-954-987B-6

Alignment Scores:
Pred. No.: 1.93 Length: 1032
Score: 98.50 Matches: 100
Percent Similarity: 37.29% Conservative: 57
Best Local Similarity: 23.75% Mismatch: 137
Query Match: 3.53% Indels: 127
DB: 11 Gaps: 27

US-09-745-506-74 (1-1553) x US-09-954-987B-6 (1-1032)
QY 251 TTGAGGCTCTCTTCTTCTGAAAT-----GACTTGCATCCCTCTCG 295
DB 336 LeuArgLysLeuAlaLeuSerPheAsnTyrGlnLysArgValSerPheAlaHisLeuSer 355
QY 296 TTTCGTGAGAGTGGCAATGTGTGATTAAGTGTGAGACCAACCCACACATACGTGA 355
DB 356 LeuAlaProSerPheGlySerLeuValAlaLeuLysGlnLeuAsp-----Met 371
QY 356 AATCACTCTTCTCGACCAAT-----GACCTGAGTGAAGAGTG 394
DB 372 HisGlyLeuPhePheArgSerLeuAspGlnThrThrLeuArgProLeuAlaArgLeuPro 391
QY 395 ATGGAGGAGGTGCTCAAAAGAGAGGACCTCATCTCTCCATCCGACCTATCTTC 454
DB 392 MetLeuGlnThrLeuArgLeuGlnMetCAsnPheIleAsnGlnAlaGlnLeuGlyIlePhe 411
QY 455 CGACCCATGAAGCCGATACCTGGAACACATGGAAGAGCCCTGTGATCCGGGCTCTG 514
DB 412 ArgAlaPheProGlyLeuArgTyr-----ValAspLeuSer 423
QY 515 GAGAACGAGCTGATCTACTCTCTCATACAGC---TATGATGCTGC3CCGACGGC 571
DB 424 AspaAsnArgLysSerGlyAlaSerGlnLeuThrAlaThrMetGlyGlnAlaAspGlyGly 443
QY 572 GTCAACAAGTGTGGCTAAAGG-----CTTGAGCTGTGTACTCCAGGCCCATCAT 625
DB 444 GlnLysValTyrLeuGlnProGlyAspLeuAlaProAlaProValAspThrProSerSer 463
QY 626 CTTTCCCAAGCTCCCACTACCCCTACAGAGGAAACCAAGTAGAATTCACGTTAAC 685
DB 464 GluAspPheArgProAsnCysSerThr-----LeuAsn 474
QY 686 TACACCAAGACCTGGACAAAGTCATGTGCACTGAAGAATTAAGCGTTTCTGTC 745
DB 475 PheThrLeuAspLeuSerArg-----AsnAsnLeuValThrValGlnPro 489
QY 746 ACTTCTTTTCTGTAGACTGTGAATGAGGAACAACAGGATTAATCTAATTTACT 805
DB 746 ACTTCTTTTCTGTAGACTGTGAATGAGGAACAACAGGATTAATCTAATTTACT 805

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DB 490 GluMetPhe--AlaGlnLeuSerHisLeuGlnCysLeuArgLeuSerHisAsnCysIle 508
QY 806 CAGAACGCTTGG-----ATGACGCTGCTGATTTT 835
DB 509 SerGlnAlaValAlaAngLysSerGlnPheLeuProLeuThrGlyLeuGlnValLeuAsp--- 527
QY 836 CTTTCCCGGACAA--CAACTTATCAGAG-----ACGAAATTCGTGTCACTG 883
DB 528 LeuSerArgAsnLysLeuAspLeuTyrHisGlnHisSerPheThrGlnLeuProArgLeu 547
QY 884 GAGAACGCTTGTCTACATAC--GAAATGGACGGTTA 922
DB 548 GlnAlaLeuAspLeuSerTyrAsnSerGlnProPheGlyMetGlnGlyValGly----- 565
QY 923 TGCACACAGATGATGATCTGTCTCCCTGCACACATGATGATGATGATGATGATGATGAT 982
DB 566 -----HisAsnPheSerPheValAlaHisLeu--ArgThrLeuArgHisLeu 580
QY 983 AAATATCTCATATTCGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCT 1042
DB 581 SerLeuAlaHis-----AsnAsnIleHisSerGlnValSer 592
QY 1043 GTCTGGCCCTGTGTCTGCTGT-----TTGGGACAGCGTT--- 1078
DB 593 --GlnGlnLeuCysSerThrSerLeuArgAlaLeuAspPheSerGlyAsnAlaLeuGly 611
QY 1079 CTCGAGGCTGTGGAGGCTGACCTTACCTGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1138
DB 612 HisMetTyrAlaGlnGlyAspLeuTyrLeu-----HisPhe----- 623
QY 1139 GATGCTGCTTCCCAAGAAATGATCATCTCTGTGAAACAGACACATGAAACAGAGC 1198
DB 624 -----PheGlnGlyLeuSerGlyLeuLe----- 631
QY 1199 TTTCTTGTGACCTTTCGAGATATGCTGATTTCTGACATGAAATGATGATGATGATGATG 1258
DB 632 -----TyrLeuAspLeuSer--GlnAsnArgLeuHisThrLeu 643
QY 1259 CTATCAGAGACTGACAGGAGC-----CCTCTGAGTGTGATTAATTCAGAAACAT 1309
DB 644 LeuProGlnThrLeuArgAsnLeuProLysSerLeuGlnValLeuArgLeu----- 660
QY 1310 CAGATTAACATATTCCTCAAAATCAGCTG-----ATGCCCAACTTAAT 1354
DB 661 ArgAspAsnTyrLeuAlaPhePheLysTyrTyrPheSerLeuHisPheLeuProLysLeuGln 680
QY 1355 TTG 1357
DB 681 Val 681

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